WHAT IS CLAIMED IS:

1. A crystal of a ribosome or a ribosomal subunit wherein the crystal has an average thickness greater than about 15 μm.

2. The crystal of claim 1 wherein the average thickness is selected from the group consisting of from about 16 μm to about 65 μm, from about 66 μm to about 105 μm, from about 104 μm to about 155 μm, and from about 156 μm to about 205 μm.

3. The crystal of claim 1 wherein the average thickness is from about 100 μm to about 200 μm.

4. An untwinned crystal of a ribosome or ribosomal subunit.

5. The crystal of claim 1 or 4 wherein the ribosomal subunit is a large ribosomal subunit.

6. The crystal of claim 1 or 4 wherein the ribosomal subunit is a small ribosomal subunit.

7. The crystal of claim 1 or 4 wherein the ribosomal subunit is a 50S ribosomal subunit.

8. The crystal of claim 1 or 4 wherein the ribosome or ribosomal subunit is obtained from a prokaryote or from an eukaryote.

9. The crystal of claim 1 or 4 wherein the ribosome or ribosomal subunit is obtained from an archaebacteria.

10. The crystal of claim 1 or 4 wherein the ribosome or ribosomal subunit is obtained from *Haloarcula marismortui*.

11. The crystal of claim 1 or 4 wherein the ribosomal subunit is a 60S ribosomal subunit.

12. The crystal of claim 1 or 4 wherein the ribosome or ribosomal subunit is obtained from a mammal.

13. The crystal of claim 1 or 4 wherein the crystal effectively diffracts X-rays for determination of atomic co-ordinates to a resolution of at least about 3.0 Å.

14. The crystal of claim 1 or 4 further comprising a ligand.

15. The crystal of claim 14 wherein the ligand is bound to the ribosome or the ribosomal subunit.

16. The crystal of claim 15 wherein the ligand is an antibiotic.

17. The crystal of claim 16 wherein the antibiotic is a macrolide antibiotic.

18. A crystal of a ribosome or a ribosomal subunit wherein the crystal effectively diffracts X-rays for determination of atomic co-ordinates to a resolution of at least about 3.0 Å.

19. A crystal of a ribosome or a ribosomal subunit wherein the crystal effectively diffracts X-rays for determination of atomic co-ordinates to a resolution of about 2.4 Å.

20. A crystal of a ribosome or a ribosomal subunit wherein the crystal is sufficient to determine the atomic co-ordinates of the ribosome or ribosomal subunit.

21. A crystal of a 50S ribosomal subunit comprising an atomic structure characterized by the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK or 1JJ2.

22. Phases computed from the co-ordinates of claim 21.

23. A method of obtaining an electron density map of a selected ribosomal subunit, wherein the selected ribosomal subunit is different from the ribosomal subunit used to obtain the computed phases of claim 22, said method comprising:

(a) producing a crystal of a selected ribosomal subunit, wherein the crystal is isomorphous;

(b) obtaining diffraction amplitudes of the crystal produced in step (a);

(c) combining the computed phases of claim 22 with the diffraction amplitudes obtained in step (b) to produce a combined data set; and

(d) obtaining an electron density map of the selected ribosomal subunit based on the combined data set obtained in step (c).

24. A method of obtaining an electron density map of a selected ribosomal subunit, wherein the selected ribosomal subunit is closely related to the ribosomal subunit used to obtain the computed phases of claim 22, said method comprising:

(a) producing a crystal of a selected ribosomal subunit, wherein the crystal crystallizes in a different unit cell with different symmetry than the crystal which was used to compute the phases of claim 22;

(b) obtaining X-ray diffraction data for the crystal produced in step (a);

(c) obtaining phases of the selected ribosomal subunit by using the data obtained in step (b) and the computed phases of claim 22 in a molecular replacement technique; and

(d) obtaining an electron density map of the selected ribosomal subunit from the phases obtained in step (c).

25. A method of obtaining a model of a selected ribosomal subunit, wherein the selected ribosomal subunit diverges from but is still homologous to the ribosomal subunit used to obtain the computed phases of claim 22, said method comprising:

(a) producing a crystal of a selected ribosomal subunit;

(b) obtaining atomic co-ordinates for the crystal produced in step (a);

(c) obtaining a model for the selected ribosomal subunit by homology modeling using the atomic co-ordinates obtained in step (b) and the computed phases of claim 22.

26. A method of growing a crystal of a ribosome or a ribosomal subunit comprising:

(a) isolating a ribosome or a ribosomal subunit;

(b) precipitating the ribosome or ribosomal subunit;

(c) back-extracting the precipitated ribosome or ribosomal subunit to obtain a solution;

(d) seeding the back-extracted solution;

(e) growing a crystal of the ribosome or ribosomal subunit from the seeded solution by vapor diffusion at room temperature; and

(f) harvesting the crystal.

27. The method of claim 26 further comprising:

(g) stabilizing the crystal by gradual transfer into a solution containing a high salt concentration; and

(h) maintaining the crystal under high salt concentration.

28. The method of claim 27 wherein the high salt concentration is from about 1.2 M salt to about 1.7 M salt.

29. The method of claim 27 further comprising:

(i) flash freezing the crystal.

30. A crystal produced by the method of claim 26, 27, 28 or 29.

31. A method of obtaining X-ray diffraction data for a crystal of a ribosome or a ribosomal subunit comprising:

(a) obtaining a crystal of a ribosome or a ribosomal subunit, wherein the crystal has one or more of the following characteristics:

(1) an average thickness of greater than 15 μm;

(2) untwinned; and

(b) using X-ray crystallography to obtain X-ray diffraction data for the crystal of the ribosome or ribosomal subunit.

32. A method of obtaining an electron density map of a ribosome or a ribosomal subunit comprising using the X-ray diffraction data obtained by the method of claim 31 to obtain an electron density map of the ribosome or ribosomal subunit.

33. A method of obtaining X-ray diffraction data for a complex of a ribosome and a ligand or a complex of a ribosomal subunit and a ligand comprising:

(a) obtaining a crystal of a ribosome or a ribosomal subunit, wherein the crystal has one or more of the following characteristics:

(1) an average thickness of greater than 15 μm;

(2) untwinned;

(b) diffusing a ligand through the crystal so that the ligand binds the ribosome or ribosomal subunit to form a complex; and

(c) using X-ray crystallography to obtain X-ray diffraction data for the complex.

34. A method of obtaining X-ray diffraction data for a complex of a ribosome and a ligand or for a ribosomal subunit and a ligand comprising:

(a) obtaining a co-crystal for a complex of a ribosome and a ligand or for a complex of a ribosomal subunit and a ligand, wherein the co-crystal has one or more of the following characteristics:

(1) an average thickness of greater than 15 μm;

(2) untwinned; and

(b) using X-ray crystallography to obtain X-ray diffraction data for the complex.

35. A method of obtaining an electron density map for a complex of a ribosome and a ligand or for a complex of a ribosomal subunit and a ligand comprising using the X-ray diffraction data obtained by the method of claim 33 or 34 to obtain an electron density map of the complex of the ribosome and the ligand or for the complex of the ribosomal subunit and the ligand.

36. The method of claim 33 or 34 wherein the ligand is an antibiotic.

37. A method of locating the attachment of a ligand to a ribosome or the attachment of a ligand to a ribosomal subunit comprising:

(a) obtaining X-ray diffraction data for a ribosome or for a ribosomal subunit according to claim 31;

(b) obtaining X-ray diffraction data for a complex of a ribosome and a ligand or for a complex of a ribosomal subunit and a ligand according to the method of claim 33 or 34;

(c) subtracting the X-ray diffraction data obtained in step (a) from the X-ray diffraction data obtained in step (b) to obtain the difference in the X-ray diffraction data;

(d) obtaining phases that correspond to X-ray diffraction data obtained in step (a) using one or more of the techniques selected from the group consisting of MIR, MIRAS and SAD;

(e) utilizing the phases obtained in step (d) and the difference in the X-ray diffraction data obtained in step (c) to compute a difference Fourier image of the ligand; and

(f) locating the attachment of the ligand to a ribosome or the attachment of the ligand to a ribosomal subunit based on the computations obtained in step (e).

38. A method of obtaining a map of a ligand attached to a ribosome or of a ligand attached to a ribosomal subunit comprising:

(a) obtaining X-ray diffraction data for a ribosome or for a ribosomal subunit according to claim 31;

(b) obtaining X-ray diffraction data for a complex of a ribosome and a ligand or a complex of a ribosomal subunit and a ligand according to the method of claim 33 or 34;

(c) obtaining phases that correspond to X-ray diffraction data obtained in step (a) using one or more of the techniques selected from the group consisting of MIR, MIRAS and SAD; and

(d) utilizing the phases obtained in step (c) and the X-ray diffraction data obtained in step (b) to compute a map of the ligand and the ribosome or of the ligand and the ribosomal subunit.

39. The method of claim 37, wherein the ligand is an antibiotic.

40. A method of obtaining a modified agent comprising:

(a) obtaining a crystal of a ribosome or of a ribosomal subunit with or without a bound agent;

(b) obtaining the atomic co-ordinates of at least a portion of the ribosome or ribosomal subunit with or without the bound agent;

(c) using the atomic co-ordinates and one or more molecular modeling techniques to determine how to modify the interaction of the agent with a ribosome or ribosomal subunit; and

(d) modifying the agent based on the determinations obtained in step (c) to produce a modified agent.

41. The method of claim 40, wherein the one or more molecular modeling techniques are selected from the group consisting of graphic molecular modeling and computational chemistry.

42. The method of claim 40 further comprising contacting the modified agent with a ribosome or ribosomal subunit and detecting the interaction of the modified agent to the ribosome or ribosomal subunit.

43. A modified agent produced by the method of claim 40 wherein the modified agent binds differently to a ribosome or ribosomal subunit than does the agent from which the modified agent was derived.

44. The modified agent of claim 43, wherein the modified agent is a therapeutic agent.

45. The method of claim 40, wherein the atomic co-ordinates of the ribosome or ribosomal subunit crystal are deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0 or 1JJ2.

46. A modified agent produced by the method of claim 40, wherein the modified agent binds differently to a ribosome or ribosomal subunit than does the agent from which the modified agent was derived.

47. A computer system comprising:

(a) a memory having stored therein data indicative of atomic co-ordinates derived from an electron density map having a resolution of at least about 4.5 Å and defining a ribofunctional locus of a large subunit of a ribosome; and

(b) a processor in electrical communication with the memory, the processor comprising a program for generating a three-dimensional model representative of the ribofunctional locus.

48. The computer system of claim 47, further comprising a device for providing a visual representation of the model.

49. The computer system of claim 47, wherein the atomic co-ordinates comprise at least a portion of the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or IJJ2.

50. The computer system of claim 47, wherein the atomic co-ordinates further define at least a portion of a protein synthesis inhibitor complexed with a ribofunctional locus.

51. The computer system of claim 50, wherein the protein synthesis inhibitor is an antibiotic.

52. The computer system of claim 51, wherein the atomic co-ordinates comprise at least a portion of the atomic co-ordinates recorded on Disk No. 3 of 3 under file number anisomycin.pdb, blasticidin.pdb, carbomycin.pdb, sparsomycin.pdb, spiramycin.pdb, tylosin.pdb, or virginiamycin.pdb.

53. The computer system of claim 47, wherein the ribofunctional locus comprises at least a portion of an active site in the ribosomal subunit.

54. The computer system of claim 53, wherein the active site comprises at least a portion of a peptidyl transferase site.

55. The computer system of claim 54, wherein the peptidyl transferase site is defined by a plurality of residues set forth in Table 5.

56. The computer system of claim 47, wherein the ribofunctional locus comprises at least a portion of an A-site.

57. The computer system of claim 56, wherein the A-site is defined by a plurality of residues set forth in Table 6.

58. The computer system of claim 47 or 56, wherein the ribofunctional locus comprises at least a portion of a P-site.

59. The computer system of claim 58, wherein the P-site is defined by a plurality of residues set forth in Table 7.

60. The computer system of claim 47 or 56, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

61. The computer system of claim 60, wherein the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

62. The computer system of claim 58, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

63. The computer system of claim 62, where the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

64. The computer system of claim 47, wherein the ribofunctional locus is defined by a plurality of residues set forth in Table 11, Table 12, Table 13, Table 14, Table 15, Table 16 or Table 17.

65. The computer system of claim 47, wherein the atomic co-ordinates are produced by molecular modeling.

66. The computer system of claim 47 or 65, wherein the atomic co-ordinates are produced by homology modeling using at least a portion of the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2.

67. The computer system of claim 47 or 65, wherein the atomic co-ordinates are produced by molecular replacement using at least a portion of the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2.

68. The computer system of claim 47, wherein the ribofunctional locus is defined by atoms of a ribosomal RNA.

69. The computer system of claim 47 or 68, wherein the ribofunctional locus is defined by atoms of a ribosomal protein.

70. The computer system of claim 47, wherein the atomic co-ordinates define a residue that is present in a ribosome of a pathogen but absent from a ribosome of a host organism.

71. The computer system of claim 70, wherein the host organism is a mammal.

72. The computer system of claim 71, wherein the mammal is a human.

73. The computer system of claim 47, wherein the atomic co-ordinates define residues that are conserved among pathogens.

74. The computer system of claim 47, further comprising a program for performing drug design.

75. A molecular model produced by the computer system of claim 47.

76. A method of identifying a candidate molecule, the method comprising the steps of:

(a) providing a molecular model of a ribofunctional locus of a large subunit of a ribosome, wherein the molecular model is based on atoms derived from an electron density map having a resolution of at least about 4.5 Å; and

(b) using the model to identify a candidate molecule having a surface complementary to the ribofunctional locus.

77. The method of claim 76, wherein the candidate molecule binds the ribofunctional locus of the large subunit of the ribosome.

78. The method of claim 76, comprising the additional step of producing the candidate molecule identified in step (b).

79. The method of claim 76 or 78, comprising the additional step of determining whether the candidate molecule modulates ribosomal activity.

80. The method of claim 79, comprising the additional step of identifying a modified molecule.

81. The method of claim 80, comprising the additional step of producing the modified molecule.

82. The method of claim 81, comprising the additional step of determining whether the modified molecule modulates ribosomal activity.

83. The method of claim 82, comprising the additional step of producing the modified molecule.

84. The method of claim 76, wherein the candidate molecule is an antibiotic or an antibiotic analogue.

85. The method of claim 80, wherein the modified molecule is an antibiotic or an antibiotic analogue.

86. The method of claim 84, wherein the antibiotic or antibiotic analogue is a macrolide.

87. The method of claim 76, wherein the ribofunctional locus comprises at least a portion of an active site.

88. The method of claim 87, wherein the active site comprises at least a portion of a peptidyl transferase site.

89. The method of claim 87, wherein the peptidyl transferase site is defined by a plurality of residues set forth in Table 5.

90. The method of claim 76, wherein the ribofunctional locus comprises at least a portion of an A-site.

91. The method of claim 90, wherein the A-site is defined by a plurality of residues set forth in Table 6.

92. The method of claim 76 or 90, wherein the ribofunctional locus comprises a least a portion of a P-site.

93. The method of claim 92, wherein the P-site is defined by a plurality of residues set forth in Table 7.

94. The method of claim 76 or 90, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

95. The method of claim 94, wherein the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

96. The method of claim 92, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

97. The method of claim 96, wherein the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

98. The method of claim 76, wherein the ribofunctional locus is defined by a plurality of residues set forth in Table 11, Table 12, Table 13, Table 14, Table 15, Table 16 or Table 17.

99. The method of claim 76, wherein the molecular model is in an electronic form.

100. The method of claim 76, wherein the molecular model is generated from atomic co-ordinates produced by molecular modeling.

101. The method of claim 76 or 100, wherein the molecular model is generated from atomic co-ordinates produced by homology modeling using at least a portion of the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2.

102. The method of claim 76 or 100, wherein the molecular model is generated from atomic co-ordinates produced by molecular replacement using at least a portion of the atomic co-ordinates deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2.

103. The method of claim 76, wherein the molecular model comprises residues that are conserved among prokaryotic organisms.

104. The method of claim 76, wherein the molecular model comprises a residue that is present in a prokaryotic ribosome but is absent from a eukaryotic ribosome.

105. The method of claim 104, wherein the eukaryotic ribosome is a mammalian ribosome.

106. An protein synthesis inhibitor comprising:

a first binding domain having a surface that mimics or duplicates a surface of a known first molecule that binds with a first contact site in a large ribosomal subunit; and

a second binding domain having a surface that mimics or duplicates a surface of a known second molecule that binds with a second contact site in the ribosomal subunit,

wherein the first domain is attached to the second domain so as to permit both the first domain and the second domain to bind with its respective contact site thereby to disrupt protein synthesis in a ribosomal subunit.

107. The inhibitor of claim 106, wherein the first molecule is a first antibiotic.

108. The inhibitor of claim 106, wherein the first antibiotic binds at least a portion of a ribofunctional locus.

109. The inhibitor of claim 106 or 107, wherein the second molecule is a second antibiotic.

110. The inhibitor of claim 109, wherein the second antibiotic binds at least a portion of a ribofunctional locus.

111. An engineered, synthetic protein synthesis inhibitor, the inhibitor comprising:

a binding domain having a surface that mimics or duplicates a surface of a known molecule which binds with a contact site in a ribosomal subunit; and

an effector domain attached to the binding domain which, upon binding of the binding domain with the contact site, occupies a space within or adjacent the ribosomal subunit thereby to disrupt protein synthesis in the ribosomal subunit.

112. The inhibitor of claim 111, wherein the surface of the binding domain mimics or duplicates a surface of a known antibiotic which binds with the contact site.